

Sequence Listing CBH 10377-WO.ST25  
SEQUENCE LISTING

&lt;110&gt; Novozymes AS

&lt;120&gt; CBHII

&lt;130&gt; 10377.204-WO

&lt;160&gt; 36

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 1731

&lt;212&gt; DNA

&lt;213&gt; Chaetomium thermophilum NP000980

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (63)..(1493)

&lt;400&gt; 1

cgggggggggg ggacagcaca acagagtcaa gacaagcttg gtcgctttgt cagaagttca 60

tc	atg	gct	aag	cag	ctg	ctg	ctc	act	gcc	gct	ctt	gcg	gcc	act	tcg			107
	Met	Ala	Lys	Gln	Leu	Leu	Leu	Thr	Ala	Ala	Leu	Ala	Ala	Thr	Ser			
	1				5					10					15			

ctg	gct	gcc	cct	ctc	ctt	gag	gag	cgc	cag	agc	tgc	tcc	tcc	gtc	tgg			155
Leu	Ala	Ala	Pro	Leu	Leu	Glu	Glu	Arg	Gln	Ser	Cys	Ser	Ser	Val	Trp			
				20					25					30				

ggt	caa	tgc	ggt	ggc	atc	aat	tac	aac	ggc	ccg	acc	tgc	tgc	cag	tcc			203
Gly	Gln	Cys	Gly	Gly	Ile	Asn	Tyr	Asn	Gly	Pro	Thr	Cys	Cys	Gln	Ser			
			35					40					45					

ggc	agt	gtt	tgc	act	tac	ctg	aat	gac	tgg	tac	agc	cag	tgc	att	ccc			251
Gly	Ser	Val	Cys	Thr	Tyr	Leu	Asn	Asp	Trp	Tyr	Ser	Gln	Cys	Ile	Pro			
		50					55					60						

ggt	cag	gct	cag	ccc	ggc	acg	act	agc	acc	acg	gct	cgg	acc	acc	agc			299
Gly	Gln	Ala	Gln	Pro	Gly	Thr	Thr	Ser	Thr	Thr	Ala	Arg	Thr	Thr	Ser			
	65					70				75								

acc	agc	acc	acc	agc	act	tcg	tcg	gtc	cgc	ccg	acc	acc	tcg	aat	acc			347
Thr	Ser	Thr	Thr	Ser	Thr	Ser	Ser	Val	Arg	Pro	Thr	Thr	Ser	Asn	Thr			
80					85					90					95			

cct	gtg	acg	act	gct	ccc	ccg	acg	acc	acc	atc	ccg	ggc	ggc	gcc	tcg			395
Pro	Val	Thr	Thr	Ala	Pro	Pro	Thr	Thr	Thr	Ile	Pro	Gly	Gly	Ala	Ser			
				100					105					110				

agc	acg	gcc	agc	tac	aac	ggc	aac	ccg	ttt	tcg	ggt	gtt	caa	ctt	tgg			443
Ser	Thr	Ala	Ser	Tyr	Asn	Gly	Asn	Pro	Phe	Ser	Gly	Val	Gln	Leu	Trp			
			115					120					125					

gcc	aac	acc	tac	tac	tcg	tcc	gag	gtg	cac	act	ttg	gcc	atc	ccc	agc			491
Ala	Asn	Thr	Tyr	Tyr	Ser	Ser	Glu	Val	His	Thr	Leu	Ala	Ile	Pro	Ser			
		130					135					140						

ttg	tct	cct	gag	ctg	gct	gcc	aag	gcc	gcc	aag	gtc	gct	gag	gtt	ccc			539
Leu	Ser	Pro	Glu	Leu	Ala	Ala	Lys	Ala	Ala	Lys	Val	Ala	Glu	Val	Pro			
	145					150					155							

agc	ttc	cag	tgg	ctc	gac	cgc	aat	gtg	act	gtt	gac	act	ctc	ttc	tcc			587
Ser	Phe	Gln	Trp	Leu	Asp	Arg	Asn	Val	Thr	Val	Asp	Thr	Leu	Phe	Ser			
160					165					170					175			

## Sequence Listing CBH 10377-WO.ST25

ggc act ctt gcc gaa atc cgc gcc gcc aac cag cgc ggt gcc aac ccg Gly Thr Leu Ala Glu Ile Arg Ala Ala Asn Gln Arg Gly Ala Asn Pro 180 185 190	635
cct tat gcc ggc att ttc gtg gtt tat gac tta cca gac cgt gat tgc Pro Tyr Ala Gly Ile Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys 195 200 205	683
gcg gct gct gct tcg aac ggc gag tgg tct atc gcc aac aat ggt gcc Ala Ala Ala Ala Ser Asn Gly Glu Trp Ser Ile Ala Asn Asn Gly Ala 210 215 220	731
aac aac tac aag cgc tac atc gac cgg atc cgt gag ctc ctt atc cag Asn Asn Tyr Lys Arg Tyr Ile Asp Arg Ile Arg Glu Leu Leu Ile Gln 225 230 235	779
tac tcc gat atc cgc act att ctg gtc att gaa cct gat tcc ctg gcc Tyr Ser Asp Ile Arg Thr Ile Leu Val Ile Glu Pro Asp Ser Leu Ala 240 245 250 255	827
aac atg gtc acc aac atg aac gtc cag aag tgc tcg aac gct gcc tcc Asn Met Val Thr Asn Met Asn Val Gln Lys Cys Ser Asn Ala Ala Ser 260 265 270	875
act tac aag gag ctt act gtc tat gcc ctc aaa cag ctc aat ctt cct Thr Tyr Lys Glu Leu Thr Val Tyr Ala Leu Lys Gln Leu Asn Leu Pro 275 280 285	923
cac gtt gcc atg tac atg gat gct ggc cac gct ggc tgg ctt ggc tgg His Val Ala Met Tyr Met Asp Ala Gly His Ala Gly Trp Leu Gly Trp 290 295 300	971
ccc gcc aac atc cag cct gct gct gag ctc ttt gct caa atc tac cgc Pro Ala Asn Ile Gln Pro Ala Ala Glu Leu Phe Ala Gln Ile Tyr Arg 305 310 315	1019
gac gct ggc agg ccc gct gct gtc cgc ggt ctt gcg acc aac gtt gcc Asp Ala Gly Arg Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala 320 325 330 335	1067
aac tac aat gct tgg tcg atc gcc agc cct ccg tcc tac acc tct cct Asn Tyr Asn Ala Trp Ser Ile Ala Ser Pro Pro Ser Tyr Thr Ser Pro 340 345 350	1115
aac ccg aac tac gac gag aag cac tat att gag gcc ttt gct cct ctt Asn Pro Asn Tyr Asp Glu Lys His Tyr Ile Glu Ala Phe Ala Pro Leu 355 360 365	1163
ctc cgc aac cag ggc ttc gac gca aag ttc atc gtc gac acc ggc cgt Leu Arg Asn Gln Gly Phe Asp Ala Lys Phe Ile Val Asp Thr Gly Arg 370 375 380	1211
aac ggc aag cag ccc act ggc cag ctt gaa tgg ggt cac tgg tgc aat Asn Gly Lys Gln Pro Thr Gly Gln Leu Glu Trp Gly His Trp Cys Asn 385 390 395	1259
gtc aag gga act ggc ttc ggt gtg cgc cct act gct aac act ggg cat Val Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ala Asn Thr Gly His 400 405 410 415	1307
gaa ctt gtt gat gct ttc gtg tgg gtc aag ccc ggt ggc gag tcc gac Glu Leu Val Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp 420 425 430	1355
ggc acc agt gcg gac acc agc gct gct cgt tat gac tat cac tgc ggc Gly Thr Ser Ala Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly 435 440 445	1403

## Sequence Listing CBH 10377-WO.ST25

ctt tcc gac gca ctg act ccg gcg cct gag gct ggc caa tgg ttc cag 1451  
 Leu Ser Asp Ala Leu Thr Pro Ala Pro Glu Ala Gly Gln Trp Phe Gln  
 450 455 460

gct tat ttc gaa cag ctg ctc atc aat gcc aac cct ccg ctc 1493  
 Ala Tyr Phe Glu Gln Leu Leu Ile Asn Ala Asn Pro Pro Leu  
 465 470 475

tgaacggaag cggagatacc ggaaggcggg gagaagagcg gaattcaagt ctgcttatca 1553

aaatccactc accaagtgga ttaaagcgga ttatacatc tgagaaacaa cctgctttaa 1613

actcttcttg tacatatctc acttcgagac gtgcctcttt ctcaggagca ctgtagatac 1673

caatatatct gtcacatttc atataaaaaa aaaaaaaaag aaaaaaagta ctagtcga 1731

<210> 2

<211> 477

<212> PRT

<213> Chaetomium thermophilum NP000980

<400> 2

Met Ala Lys Gln Leu Leu Leu Thr Ala Ala Leu Ala Ala Thr Ser Leu  
 1 5 10 15

Ala Ala Pro Leu Leu Glu Glu Arg Gln Ser Cys Ser Ser Val Trp Gly  
 20 25 30

Gln Cys Gly Gly Ile Asn Tyr Asn Gly Pro Thr Cys Cys Gln Ser Gly  
 35 40 45

Ser Val Cys Thr Tyr Leu Asn Asp Trp Tyr Ser Gln Cys Ile Pro Gly  
 50 55 60

Gln Ala Gln Pro Gly Thr Thr Ser Thr Thr Ala Arg Thr Thr Ser Thr  
 65 70 75 80

Ser Thr Thr Ser Thr Ser Ser Val Arg Pro Thr Thr Ser Asn Thr Pro  
 85 90 95

Val Thr Thr Ala Pro Pro Thr Thr Thr Ile Pro Gly Gly Ala Ser Ser  
 100 105 110

Thr Ala Ser Tyr Asn Gly Asn Pro Phe Ser Gly Val Gln Leu Trp Ala  
 115 120 125

Asn Thr Tyr Tyr Ser Ser Glu Val His Thr Leu Ala Ile Pro Ser Leu  
 130 135 140

Ser Pro Glu Leu Ala Ala Lys Ala Ala Lys Val Ala Glu Val Pro Ser  
 145 150 155 160

Phe Gln Trp Leu Asp Arg Asn Val Thr Val Asp Thr Leu Phe Ser Gly  
 165 170 175

## Sequence Listing CBH 10377-WO.ST25

Thr Leu Ala Glu Ile Arg Ala Ala Asn Gln Arg Gly Ala Asn Pro Pro  
 180 185 190  
 Tyr Ala Gly Ile Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala  
 195 200 205  
 Ala Ala Ala Ser Asn Gly Glu Trp Ser Ile Ala Asn Asn Gly Ala Asn  
 210 215 220  
 Asn Tyr Lys Arg Tyr Ile Asp Arg Ile Arg Glu Leu Leu Ile Gln Tyr  
 225 230 235 240  
 Ser Asp Ile Arg Thr Ile Leu Val Ile Glu Pro Asp Ser Leu Ala Asn  
 245 250 255  
 Met Val Thr Asn Met Asn Val Gln Lys Cys Ser Asn Ala Ala Ser Thr  
 260 265 270  
 Tyr Lys Glu Leu Thr Val Tyr Ala Leu Lys Gln Leu Asn Leu Pro His  
 275 280 285  
 Val Ala Met Tyr Met Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro  
 290 295 300  
 Ala Asn Ile Gln Pro Ala Ala Glu Leu Phe Ala Gln Ile Tyr Arg Asp  
 305 310 315 320  
 Ala Gly Arg Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn  
 325 330 335  
 Tyr Asn Ala Trp Ser Ile Ala Ser Pro Pro Ser Tyr Thr Ser Pro Asn  
 340 345 350  
 Pro Asn Tyr Asp Glu Lys His Tyr Ile Glu Ala Phe Ala Pro Leu Leu  
 355 360 365  
 Arg Asn Gln Gly Phe Asp Ala Lys Phe Ile Val Asp Thr Gly Arg Asn  
 370 375 380  
 Gly Lys Gln Pro Thr Gly Gln Leu Glu Trp Gly His Trp Cys Asn Val  
 385 390 395 400  
 Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ala Asn Thr Gly His Glu  
 405 410 415  
 Leu Val Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly  
 420 425 430  
 Thr Ser Ala Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu  
 435 440 445

## Sequence Listing CBH 10377-WO.ST25

Ser Asp Ala Leu Thr Pro Ala Pro Glu Ala Gly Gln Trp Phe Gln Ala  
 450 455 460

Tyr Phe Glu Gln Leu Leu Ile Asn Ala Asn Pro Pro Leu  
 465 470 475

<210> 3  
 <211> 1272  
 <212> DNA  
 <213> Myceliophthora thermophila

<220>  
 <221> misc\_feature  
 <222> (61)..(61)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (87)..(87)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (420)..(420)  
 <223> n is a, c, g, or t

<400> 3  
 acgtggatcc gaattcaagc ttcattgggggt tctcctgcga tccactagta acggctcgcc 60  
 ngagagctgg aaagccagca gcacctnttg gagaggcagc tctctctctc caccacgccc 120  
 ccgcccgtct ccagccctcg tgaccagcat tcccggcggg gcgacctcca cggcgagcta 180  
 ctctggcaac cccttctcgg gcgtccgggt cttcgccaac gactactaca ggtccgaggt 240  
 ccacaatctc gccattccta gcatgactgg tactctggcg gctcaaggct tccgccgtcg 300  
 cgcggaagtcc ctagcttcca gtggctcgac acggaacgtg cactcatcag acaccctgat 360  
 ggtccagact ctgtaccag gtccgggctc tcaataaggc acggtgaaca atcctaccn 420  
 tatgctgccc aactcgtcgt ctacgacctc cccgaccgtg actgtgccgc cgctgcgtcc 480  
 aacggygagt tttcgattgc aaacggcggc gccgccaact acaggagcta catcgacgct 540  
 atccgcaagc acatcattga gtactcggac atccggatca tcctggttat cgagcccagc 600  
 tcgatggcca acatggtgac caacatgaac gtggccaagt gcagcaacgc cgcgtcgacg 660  
 taccacgagt tgaccgtgta cgcgtcaag cagctgaacc tgcccaacgt cgccatgtat 720  
 ctcgacgccg gccacgccgg ctggctcggc tggcccgcga acatccagcc cgccgccgag 780  
 ctgtttgccc gcatctacaa tgatgccggc aagccgggtg ccgtccgcgg cctggccact 840  
 aacgtcgcca actacaacgc ctggagcatc gtttcggccc cgtcgtacac gtcgggtaac 900  
 cctaactacg acgagaagca ctacatcgag gccttcagcc cgctcttgaa ctcggccggc 960  
 ttccccgcac gtttcattgt cgacactggc cgcaacggca aacaacctac cggccaacaa 1020  
 cagtggggcg actggtgcaa tgtcaagggc accggctttg gcgtgcgccc gacggccaac 1080  
 acgggccacg agctggtcga tgcctttgtc tgggtcaagc ccggcggcga gtccgacggc 1140

## Sequence Listing CBH 10377-WO.ST25

acaagcgaca ccagcgccgc ccgctacgac taccactgcg gcctgtccga tgccctgcag 1200  
 cctgcccccg aggctggaca gtggttccag gcctacttcg agcagctgct caccaacgcc 1260  
 aaccgcct tc 1272

<210> 4  
 <211> 420  
 <212> PRT  
 <213> Myceliophthora thermophila  
 <400> 4

Thr Trp Ile Arg Ile Gln Ala Ser Trp Gly Ser Pro Ala Ile His Arg  
 1 5 10 15

Leu Ala Glu Leu Glu Ser Gln Gln His Leu Leu Glu Arg Gln Leu Ser  
 20 25 30

Leu Ser Thr Thr Pro Pro Pro Val Ser Ser Pro Arg Asp Gln His Ser  
 35 40 45

Arg Arg Cys Asp Leu His Gly Glu Leu Leu Trp Gln Pro Leu Leu Gly  
 50 55 60

Arg Pro Ala Leu Arg Gln Arg Leu Leu Gln Val Arg Gly Pro Gln Ser  
 65 70 75 80

Arg His Ser His Asp Trp Tyr Ser Gly Gly Ser Arg Leu Pro Pro Ser  
 85 90 95

Arg Glu Val Pro Ser Phe Gln Trp Leu Asp Thr Glu Arg Ala Leu Ile  
 100 105 110

Arg His Pro Asp Gly Pro Asp Ser Val Pro Arg Ser Gly Leu Ser Ile  
 115 120 125

Arg His Gly Glu Gln Ser Tyr Pro Tyr Ala Ala Gln Leu Val Val Tyr  
 130 135 140

Asp Leu Pro Asp Arg Asp Cys Ala Ala Ala Ala Ser Asn Gly Glu Phe  
 145 150 155 160

Ser Ile Ala Asn Gly Gly Ala Ala Asn Tyr Arg Ser Tyr Ile Asp Ala  
 165 170 175

Ile Arg Lys His Ile Ile Glu Tyr Ser Asp Ile Arg Ile Ile Leu Val  
 180 185 190

Ile Glu Pro Asp Ser Met Ala Asn Met Val Thr Asn Met Asn Val Ala  
 195 200 205

Lys Cys Ser Asn Ala Ala Ser Thr Tyr His Glu Leu Thr Val Tyr Ala

## Sequence Listing CBH 10377-WO.ST25

210

215

220

Leu Lys Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly  
 225 230 235 240

His Ala Gly Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Glu  
 245 250 255

Leu Phe Ala Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ala Val Arg  
 260 265 270

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Ile Ala Ser  
 275 280 285

Ala Pro Ser Tyr Thr Ser Ala Asn Pro Asn Tyr Asp Glu Lys His Tyr  
 290 295 300

Ile Glu Ala Phe Ser Pro Leu Leu Asn Ser Ala Gly Phe Pro Ala Arg  
 305 310 315 320

Phe Ile Val Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln  
 325 330 335

Gln Trp Gly Asp Trp Cys Asn Val Lys Gly Thr Gly Phe Gly Val Arg  
 340 345 350

Pro Thr Ala Asn Thr Gly His Glu Leu Val Asp Ala Phe Val Trp Val  
 355 360 365

Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Ala Arg  
 370 375 380

Tyr Asp Tyr His Cys Gly Leu Ser Asp Ala Leu Gln Pro Ala Pro Glu  
 385 390 395 400

Ala Gly Gln Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu Thr Asn Ala  
 405 410 415

Asn Pro Pro Phe  
 420

<210> 5  
 <211> 419  
 <212> DNA  
 <213> Acremonium sp.T178-4 NP001132

<220>  
 <221> CDS  
 <222> (1)..(417)

<400> 5  
 tac gca agt gtc tac tcg gac gcc gga tca ccg gct gca ctc cgc ggt  
 Tyr Ala Ser Val Tyr Ser Asp Ala Gly Ser Pro Ala Ala Leu Arg Gly

## Sequence Listing CBH 10377-WO.ST25

1                      5                      10                      15

ctc gct acc aac gtc gcc aat tac aac gcc tgg aca atc gat acc tgc      96  
 Leu Ala Thr Asn Val Ala Asn Tyr Asn Ala Trp Thr Ile Asp Thr Cys  
                     20                      25                      30

cct tca tac aca cag ggt aac tcc att tgc gac gag aag gac tac atc      144  
 Pro Ser Tyr Thr Gln Gly Asn Ser Ile Cys Asp Glu Lys Asp Tyr Ile  
                     35                      40                      45

aat gcg ctt gct ccc ctg ctt cgc agc tca ggg ctt acg gac gct cat      192  
 Asn Ala Leu Ala Pro Leu Leu Arg Ser Ser Gly Leu Thr Asp Ala His  
                     50                      55                      60

ttc atc act gat acc ggc cgc aac ggc aag caa cca aca ggc caa caa      240  
 Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln  
                     65                      70                      75                      80

gcc tgg ggc gac tgg tgc aat gtc atc ggc acg ggc ttt ggc gtg cgc      288  
 Ala Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Val Arg  
                     85                      90                      95

ccg tcc acg aac aca ggt gat tct tta ctt gac gcc ttc gtc tgg gtt      336  
 Pro Ser Thr Asn Thr Gly Asp Ser Leu Leu Asp Ala Phe Val Trp Val  
                     100                      105                      110

aaa ccc ggt ggc gag agt gac ggg act tct gat act tgt gcg gcg cgg      384  
 Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Cys Ala Ala Arg  
                     115                      120                      125

tat gat gcg cat tgc ggg tat agc gat gcg ctg ca      419  
 Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu  
                     130                      135

<210> 6  
 <211> 139  
 <212> PRT  
 <213> Acremonium sp.T178-4 NP001132.

<400> 6

Tyr Ala Ser Val Tyr Ser Asp Ala Gly Ser Pro Ala Ala Leu Arg Gly  
 1                      5                      10                      15

Leu Ala Thr Asn Val Ala Asn Tyr Asn Ala Trp Thr Ile Asp Thr Cys  
                     20                      25                      30

Pro Ser Tyr Thr Gln Gly Asn Ser Ile Cys Asp Glu Lys Asp Tyr Ile  
                     35                      40                      45

Asn Ala Leu Ala Pro Leu Leu Arg Ser Ser Gly Leu Thr Asp Ala His  
                     50                      55                      60

Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln  
 65                      70                      75                      80

Ala Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Val Arg  
                     85                      90                      95

Pro Ser Thr Asn Thr Gly Asp Ser Leu Leu Asp Ala Phe Val Trp Val  
                     100                      105                      110



## Sequence Listing CBH 10377-WO.ST25

Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Cys Ala Ala Arg  
 115 120 125

Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu  
 130 135

<210> 7  
 <211> 306  
 <212> DNA  
 <213> Melanocarpus sp. AT181-3 NP001133

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 7  
 gat gcc ggc aag ccg cac tcg gtc cgc ggt ctc gcc acc aac gtc gcc 48  
 Asp Ala Gly Lys Pro His Ser Val Arg Gly Leu Ala Thr Asn Val Ala  
 1 5 10 15  
 aac tac aat gcc tgg agc gtc gcc tcg gcc ccg cct tac acc agc ccc 96  
 Asn Tyr Asn Ala Trp Ser Val Ala Ser Ala Pro Pro Tyr Thr Ser Pro  
 20 25 30  
 aac ccc aac tac gat gag aag cac tac att gag gcc ttc agc cct ctc 144  
 Asn Pro Asn Tyr Asp Glu Lys His Tyr Ile Glu Ala Phe Ser Pro Leu  
 35 40 45  
 ctt gag gcc cgc ggc ttc cct gcc cgc ttc atc gtc gac cag ggc cgc 192  
 Leu Glu Ala Arg Gly Phe Pro Ala Arg Phe Ile Val Asp Gln Gly Arg  
 50 55 60  
 agc ggc aag cag ccc acc ggc cag aag gag tgg ggc cac tgg tgc aac 240  
 Ser Gly Lys Gln Pro Thr Gly Gln Lys Glu Trp Gly His Trp Cys Asn  
 65 70 75 80  
 gct atc ggc acc ggc ttc ggc att cgc ccg acc gcc aac acc ggc cac 288  
 Ala Ile Gly Thr Gly Phe Gly Ile Arg Pro Thr Ala Asn Thr Gly His  
 85 90 95  
 aac ctg gtt gat gcc ttc 306  
 Asn Leu Val Asp Ala Phe  
 100

<210> 8  
 <211> 102  
 <212> PRT  
 <213> Melanocarpus sp. AT181-3 NP001133

<400> 8

Asp Ala Gly Lys Pro His Ser Val Arg Gly Leu Ala Thr Asn Val Ala  
 1 5 10 15

Asn Tyr Asn Ala Trp Ser Val Ala Ser Ala Pro Pro Tyr Thr Ser Pro  
 20 25 30

Asn Pro Asn Tyr Asp Glu Lys His Tyr Ile Glu Ala Phe Ser Pro Leu  
 35 40 45

## Sequence Listing CBH 10377-WO.ST25

Leu Glu Ala Arg Gly Phe Pro Ala Arg Phe Ile Val Asp Gln Gly Arg  
 50 55 60

Ser Gly Lys Gln Pro Thr Gly Gln Lys Glu Trp Gly His Trp Cys Asn  
 65 70 75 80

Ala Ile Gly Thr Gly Phe Gly Ile Arg Pro Thr Ala Asn Thr Gly His  
 85 90 95

Asn Leu Val Asp Ala Phe  
 100

<210> 9  
 <211> 432  
 <212> DNA  
 <213> Thielavia cf. microspora T046-1 NP001134

<220>  
 <221> CDS  
 <222> (1)..(432)

<400> 9  
 gcc aac atc cag ccc gct gcc acc ctg ttc gcc ggc atc tac agc gac 48  
 Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala Gly Ile Tyr Ser Asp  
 1 5 10 15  
 gct ggc aag ccc gcc tcg gtc cgc ggt ttg gcc acc aac gtg gcc aac 96  
 Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala Thr Asn Val Ala Asn  
 20 25 30  
 tac aac gcc tgg agc ctg tcg tcg gcg ccg tcg tac acg agc ccc aac 144  
 Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser Tyr Thr Ser Pro Asn  
 35 40 45  
 gcc aac tac gac gag aag cac tac gtc gag gcc ttt gcc ccg ctc ctc 192  
 Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala Phe Ala Pro Leu Leu  
 50 55 60  
 cag gcg gcc ggc ttc ccc gcc aag ttc atc acc gac acg ggc cgc aac 240  
 Gln Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr Asp Thr Gly Arg Asn  
 65 70 75 80  
 ggc aag cag ccc acg ggc cag agc gcg tgg ggc gac tgg tgc aac gtc 288  
 Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val  
 85 90 95  
 aag ggc acc ggc ttc ggt gtc cgc ccg acc tcg gag acg ggc cac gac 336  
 Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser Glu Thr Gly His Asp  
 100 105 110  
 ctc ctc gac gcc ttc gtc tgg gtc aag ccc ggt ggc gag tcg gac ggc 384  
 Leu Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly  
 115 120 125  
 acc agc gac acc agc gcc gcc cgc tac gac tac cac tgc ggt ctg tcg 432  
 Thr Ser Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu Ser  
 130 135 140

<210> 10  
 <211> 144  
 <212> PRT

## Sequence Listing CBH 10377-WO.ST25

&lt;213&gt; Thielavia cf. microspora T046-1 NP001134

&lt;400&gt; 10

Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala Gly Ile Tyr Ser Asp  
1 5 10 15Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala Thr Asn Val Ala Asn  
20 25 30Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser Tyr Thr Ser Pro Asn  
35 40 45Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala Phe Ala Pro Leu Leu  
50 55 60Gln Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr Asp Thr Gly Arg Asn  
65 70 75 80Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val  
85 90 95Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser Glu Thr Gly His Asp  
100 105 110Leu Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly  
115 120 125Thr Ser Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu Ser  
130 135 140

&lt;210&gt; 11

&lt;211&gt; 297

&lt;212&gt; DNA

&lt;213&gt; Aspergillus sp. T186-2 NP001136

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(297)

&lt;400&gt; 11

gga ttg ttt ggg tgg cct gcc aac ctt act cct tcc gct cgt ctc ttc 48  
Gly Leu Phe Gly Trp Pro Ala Asn Leu Thr Pro Ser Ala Arg Leu Phe  
1 5 10 15gcc caa atc tac aag gat gcc ggc agg tct gcc ttc atc cgt ggt ctt 96  
Ala Gln Ile Tyr Lys Asp Ala Gly Arg Ser Ala Phe Ile Arg Gly Leu  
20 25 30gcc acc aac gtc tcc aac tac aac gcc ctc agt gca acc acc cgt gat 144  
Ala Thr Asn Val Ser Asn Tyr Asn Ala Leu Ser Ala Thr Thr Arg Asp  
35 40 45ccc gtc acc cag ggc aat gac aac tac gat gag ctc cgc ttc atc aac 192  
Pro Val Thr Gln Gly Asn Asp Asn Tyr Asp Glu Leu Arg Phe Ile Asn  
50 55 60

gct ctt gct cct ctc ctc cga aat gaa ggc tgg gac gcc aag ttc atc 240

## Sequence Listing CBH 10377-WO.ST25

Ala Leu Ala Pro Leu Leu Arg Asn Glu Gly Trp Asp Ala Lys Phe Ile  
65 70 75 80

gtc gac cag ggt cgt tct ggt gtc cag aac atc cga cag gag tgg ggc 288  
Val Asp Gln Gly Arg Ser Gly Val Gln Asn Ile Arg Gln Glu Trp Gly 95

gac tgg tgc 297  
Asp Trp Cys

<210> 12  
<211> 99  
<212> PRT  
<213> *Aspergillus* sp. T186-2 NP001136

<400> 12

Gly Leu Phe Gly Trp Pro Ala Asn Leu Thr Pro Ser Ala Arg Leu Phe  
1 5 10 15

Ala Gln Ile Tyr Lys Asp Ala Gly Arg Ser Ala Phe Ile Arg Gly Leu  
20 25 30

Ala Thr Asn Val Ser Asn Tyr Asn Ala Leu Ser Ala Thr Thr Arg Asp  
35 40 45

Pro Val Thr Gln Gly Asn Asp Asn Tyr Asp Glu Leu Arg Phe Ile Asn  
50 55 60

Ala Leu Ala Pro Leu Leu Arg Asn Glu Gly Trp Asp Ala Lys Phe Ile  
65 70 75 80

Val Asp Gln Gly Arg Ser Gly Val Gln Asn Ile Arg Gln Glu Trp Gly  
85 90 95

Asp Trp Cys

<210> 13  
<211> 420  
<212> DNA  
<213> *Thielavia* cf. *australiensis* T55-15 NP001000

<220>  
<221> CDS  
<222> (1)..(420)

<400> 13 48  
tgg ctg ggg tgg ccc gcc aac atc cag ccc gct gct acc ctg ttc gcc  
Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala  
1 5 10 15

ggc atc tac aac gac gct ggc aag ccc gcc tcg gtc cgt ggt ctg gcc 96  
Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala  
20 25 30

acc aac gtt gcc aac tac aac gcc tgg agc ctg tcc tcg gcc ccg tcg 144  
Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser

## Sequence Listing CBH 10377-WO.ST25

35	40	45	
tac acg acc ccc aac gcc aac tac gac gag aag cac tac gtc gag gcc			192
Tyr Thr 50 Thr Pro Asn Ala 55 Tyr Asp Glu Lys 60 His Tyr Val Glu Ala			
ttt gcc ccg ctt ctc tcg gcc gct ggc ttc ccc gcc aag ttc atc acc			240
Phe Ala 65 Pro Leu Leu 70 Ser Ala Ala Gly Phe 75 Ala Lys Phe Ile Thr 80			
gac act ggc cgc aac ggc aag cag ccc acc ggc cag agc cag tgg ggc			288
Asp Thr 85 Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Ser Gln Trp Gly			
gat tgg tgc aac gtc aag ggc acc ggc ttc ggt gtc cgc ccg acc tcc			336
Asp Trp 100 Cys Asn Val Lys Gly Thr 105 Gly Phe Gly Val Arg Pro Thr Ser			
gag acg ggc cac gag ctc ctg gat gcc ttt gtc tgg gcc aag ccc ggt			384
Glu Thr 115 Gly His Glu Leu Leu 120 Asp Ala Phe Val Trp Ala Lys Pro Gly			
ggc gag tcc gac ggt acc agc gac acc agc gct gcc			420
Gly Glu 130 Ser Asp Gly Thr 135 Ser Asp Thr Ser Ala Ala 140			

&lt;210&gt; 14

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Thielavia cf. australiensis T55-15 NP001000

&lt;400&gt; 14

Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala  
1 5 10 15

Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala  
20 25 30

Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser  
35 40 45

Tyr Thr Thr Pro Asn Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala  
50 55 60

Phe Ala Pro Leu Leu Ser Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr  
65 70 75 80

Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Ser Gln Trp Gly  
85 90 95

Asp Trp Cys Asn Val Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser  
100 105 110

Glu Thr Gly His Glu Leu Leu Asp Ala Phe Val Trp Ala Lys Pro Gly  
115 120 125

Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Ala  
130 135 140

## Sequence Listing CBH 10377-WO.ST25

<210> 15  
 <211> 1221  
 <212> DNA  
 <213> *Aspergillus tubingensis* NP001143

<220>  
 <221> CDS  
 <222> (1)..(1221)

<220>  
 <221> misc\_feature  
 <222> (903)..(903)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (1011)..(1011)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (1017)..(1017)  
 <223> n is a, c, g, or t

<400> 15		
atg aat atg cac tcc atc aac atg cga gcc atc tgg ccc ctc gtc tct		48
Met Asn Met His Ser Ile Asn Met Arg Ala Ile Trp Pro Leu Val Ser		
1 5 10 15		
ctc ttc tct gcc gtt aag gcc ctc ccc gcc gca agc gcg act gct tca		96
Leu Phe Ser Ala Val Lys Ala Leu Pro Ala Ala Ser Ala Thr Ala Ser		
20 25 30		
gcg tct gtt gcg gcc tcg agc tct ccg gcg ccg act gcc tct gct acc		144
Ala Ser Val Ala Ala Ser Ser Ser Pro Ala Pro Thr Ala Ser Ala Thr		
35 40 45		
ggc aat ccc ttt gag gga tac cag ctc tat gtg aac ccc tac tat aag		192
Gly Asn Pro Phe Glu Gly Tyr Gln Leu Tyr Val Asn Pro Tyr Tyr Lys		
50 55 60		
tcg caa gtg gag agt tcg gcc att cca tca ttg tct gct agt tcg ctg		240
Ser Gln Val Glu Ser Ser Ala Ile Pro Ser Leu Ser Ala Ser Ser Leu		
65 70 75 80		
gtc gcg cag gcg agt gct gca gcc gat gtg cct tca ttt tac tgg cta		288
Val Ala Gln Ala Ser Ala Ala Ala Asp Val Pro Ser Phe Tyr Trp Leu		
85 90 95		
gac acg gcc gac aag gtg cct acc atg ggt gaa tat ctg gat gac atc		336
Asp Thr Ala Asp Lys Val Pro Thr Met Gly Glu Tyr Leu Asp Asp Ile		
100 105 110		
cag acg caa aac gcc gct gga gcg aat cct ccc att gct ggt atc ttc		384
Gln Thr Gln Asn Ala Ala Gly Ala Asn Pro Pro Ile Ala Gly Ile Phe		
115 120 125		
gtc gtc tat gac ctg ccg gat cgg gat tgc gct gcc ttg gct agt aat		432
Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn		
130 135 140		
ggg gaa tac gcg atc agt gat gga ggc gtg gag aag tat aag gcg tac		480
Gly Glu Tyr Ala Ile Ser Asp Gly Gly Val Glu Lys Tyr Lys Ala Tyr		
145 150 155 160		

Sequence Listing CBH 10377-WO.ST25

att gat tct att cgc gag cag gtc gag acg tac tcg gat gtt cag act	528
Ile Asp Ser Ile Arg Glu Gln Val Glu Thr Tyr Ser Asp Val Gln Thr	
165 170 175	
att ttg att atc gaa ccg gat agc tta gct aac ctg gtg acg aat ctc	576
Ile Leu Ile Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu	
180 185 190	
gat gtg gct aaa tgc gcc aat gct caa tct gct tac ctg gaa tgc acc	624
Asp Val Ala Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Thr	
195 200 205	
aat tat gca ctt gag cag ttg aat ctr ccg aac gtg gct atg tat ctt	672
Asn Tyr Ala Leu Glu Gln Leu Asn Xaa Pro Asn Val Ala Met Tyr Leu	
210 215 220	
gat gct ggc cat gct gga tgg ctg gga tgg cct gcc aac atc ggt ccc	720
Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Ile Gly Pro	
225 230 235 240	
gcg gcg gaa ctc tac gca tcg gtg tat aag aat gcg tcg tct cca gca	768
Ala Ala Glu Leu Tyr Ala Ser Val Tyr Lys Asn Ala Ser Ser Pro Ala	
245 250 255	
gct gtt cgt gga ctc gct aca rac gta gct aac ttc aat gcc tgg agc	816
Ala Val Arg Gly Leu Ala Thr Xaa Val Ala Asn Phe Asn Ala Trp Ser	
260 265 270	
atc gac act tgc ccc tcc tat acw tcg ggt aac gat gtc tgt gat gaa	864
Ile Asp Thr Cys Pro Ser Tyr Xaa Ser Gly Asn Asp Val Cys Asp Glu	
275 280 285	
aaa agc tac atc aat gcc ttt gca ccg gag ctc tct agn gct gga ttt	912
Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu Ser Xaa Ala Gly Phe	
290 295 300	
gat gcc cac ttt att acc gat acg ggt cgc aat gga aag cag cct act	960
Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr	
305 310 315 320	
gga caa agc gcg tgg ggt gac tgg ggc aat gtc aag gat act ggc ttc	1008
Gly Gln Ser Ala Trp Gly Asp Trp Gly Asn Val Lys Asp Thr Gly Phe	
325 330 335	
ggn gct can ccg aca acc gat act gga aac gag ctg gct gat gcc ttt	1056
Gly Ala Xaa Pro Thr Thr Asp Thr Gly Asn Glu Leu Ala Asp Ala Phe	
340 345 350	
gtc tgg gyc aac cct ggc gga aag agt gat ggg acg tcg gac act agc	1104
Val Trp Xaa Asn Pro Gly Gly Lys Ser Asp Gly Thr Ser Asp Thr Ser	
355 360 365	
tct tct cgc tac gat gcg cat tgc gga tat agt gat gct ttg cag cct	1152
Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu Gln Pro	
370 375 380	
gcc ccg gag gct ggt act tgg ttc cag gca tac ttt gag cag ctt ttg	1200
Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu	
385 390 395 400	
acc aat gcc aac cct tcc ctg	1221
Thr Asn Ala Asn Pro Ser Leu	
405	

<210> 16  
 <211> 407  
 <212> PRT

## Sequence Listing CBH 10377-WO.ST25

<213> Aspergillus tubingensis NP001143

<220>

<221> misc\_feature

<222> (217)..(217)

<223> The 'Xaa' at location 217 stands for Leu.

<220>

<221> misc\_feature

<222> (264)..(264)

<223> The 'Xaa' at location 264 stands for Asp, or Asn.

<220>

<221> misc\_feature

<222> (280)..(280)

<223> The 'Xaa' at location 280 stands for Thr.

<220>

<221> misc\_feature

<222> (301)..(301)

<223> The 'Xaa' at location 301 stands for Arg, or Ser.

<220>

<221> misc\_feature

<222> (339)..(339)

<223> The 'Xaa' at location 339 stands for Gln, or His.

<220>

<221> misc\_feature

<222> (355)..(355)

<223> The 'Xaa' at location 355 stands for Ala, or Val.

<400> 16

Met Asn Met His Ser Ile Asn Met Arg Ala Ile Trp Pro Leu Val Ser  
1 5 10 15

Leu Phe Ser Ala Val Lys Ala Leu Pro Ala Ala Ser Ala Thr Ala Ser  
20 25 30

Ala Ser Val Ala Ala Ser Ser Ser Pro Ala Pro Thr Ala Ser Ala Thr  
35 40 45

Gly Asn Pro Phe Glu Gly Tyr Gln Leu Tyr Val Asn Pro Tyr Tyr Lys  
50 55 60

Ser Gln Val Glu Ser Ser Ala Ile Pro Ser Leu Ser Ala Ser Ser Leu  
65 70 75 80

Val Ala Gln Ala Ser Ala Ala Ala Asp Val Pro Ser Phe Tyr Trp Leu  
85 90 95

Asp Thr Ala Asp Lys Val Pro Thr Met Gly Glu Tyr Leu Asp Asp Ile  
100 105 110

Gln Thr Gln Asn Ala Ala Gly Ala Asn Pro Pro Ile Ala Gly Ile Phe  
115 120 125

Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn  
130 135 140



## Sequence Listing CBH 10377-WO.ST25

Gly Glu Tyr Ala Ile Ser Asp Gly Gly Val Glu Lys Tyr Lys Ala Tyr  
 145 150 155 160  
 Ile Asp Ser Ile Arg Glu Gln Val Glu Thr Tyr Ser Asp Val Gln Thr  
 165 170 175  
 Ile Leu Ile Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu  
 180 185 190  
 Asp Val Ala Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Thr  
 195 200 205  
 Asn Tyr Ala Leu Glu Gln Leu Asn Xaa Pro Asn Val Ala Met Tyr Leu  
 210 215 220  
 Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Ile Gly Pro  
 225 230 235 240  
 Ala Ala Glu Leu Tyr Ala Ser Val Tyr Lys Asn Ala Ser Ser Pro Ala  
 245 250 255  
 Ala Val Arg Gly Leu Ala Thr Xaa Val Ala Asn Phe Asn Ala Trp Ser  
 260 265 270  
 Ile Asp Thr Cys Pro Ser Tyr Xaa Ser Gly Asn Asp Val Cys Asp Glu  
 275 280 285  
 Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu Ser Xaa Ala Gly Phe  
 290 295 300  
 Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr  
 305 310 315 320  
 Gly Gln Ser Ala Trp Gly Asp Trp Gly Asn Val Lys Asp Thr Gly Phe  
 325 330 335  
 Gly Ala Xaa Pro Thr Thr Asp Thr Gly Asn Glu Leu Ala Asp Ala Phe  
 340 345 350  
 Val Trp Xaa Asn Pro Gly Gly Lys Ser Asp Gly Thr Ser Asp Thr Ser  
 355 360 365  
 Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu Gln Pro  
 370 375 380  
 Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu  
 385 390 395 400  
 Thr Asn Ala Asn Pro Ser Leu  
 405

## Sequence Listing CBH 10377-WO.ST25

<210> 17  
 <211> 429  
 <212> DNA  
 <213> Gloeophyllum trabeum NP001144

<220>  
 <221> CDS  
 <222> (1)..(429)

<400> 17  
 gca tcg tct cca gca gct gtt cgt gga ctc gct aca aac gta gct aac 48  
 Ala Ser Ser Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn  
 1 5 10 15  
 ttc aat gcc tgg agc atc gac act tgc ccc tcc tat aca tcg ggt aac 96  
 Phe Asn Ala Trp Ser Ile Asp Thr Cys Pro Ser Tyr Thr Ser Gly Asn  
 20 25 30  
 gat gtc tgt gat gag aag agc tac atc aat gcc ttt gca ccg gag ctc 144  
 Asp Val Cys Asp Glu Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu  
 35 40 45  
 tct agt gct gga ttt gat gcc cac ttt att acc gat acg ggt cgc aat 192  
 Ser Ser Ala Gly Phe Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn  
 50 55 60  
 gga aag cag cct act gga cag agc gcg tgg ggt gac tgg tgc aat gtc 240  
 Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val  
 65 70 75 80  
 aag gat act ggc ttc ggt gct cag ccg acg acc gat act gga gac gag 288  
 Lys Asp Thr Gly Phe Gly Ala Gln Pro Thr Thr Asp Thr Gly Asp Glu  
 85 90 95  
 ctg gct gat gcc ttt gtc tgg gtc aag cct ggc gga gag agt gat ggg 336  
 Leu Ala Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly  
 100 105 110  
 acg tcg gac act agc tct tct cgc tac gat gcg cat tgc gga tat agt 384  
 Thr Ser Asp Thr Ser Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser  
 115 120 125  
 gat gct ttg cag cct gcc ccg gag gct ggt act tgg ttc caa ggc 429  
 Asp Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Gly  
 130 135 140

<210> 18  
 <211> 143  
 <212> PRT  
 <213> Gloeophyllum trabeum NP001144

<400> 18  
 Ala Ser Ser Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn  
 1 5 10 15  
 Phe Asn Ala Trp Ser Ile Asp Thr Cys Pro Ser Tyr Thr Ser Gly Asn  
 20 25 30  
 Asp Val Cys Asp Glu Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu  
 35 40 45

## Sequence Listing CBH 10377-WO.ST25

Ser Ser Ala Gly Phe Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn  
 50 55 60

Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val  
 65 70 75 80

Lys Asp Thr Gly Phe Gly Ala Gln Pro Thr Thr Asp Thr Gly Asp Glu  
 85 90 95

Leu Ala Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly  
 100 105 110

Thr Ser Asp Thr Ser Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser  
 115 120 125

Asp Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Gly  
 130 135 140

<210> 19  
 <211> 213  
 <212> DNA  
 <213> Meripilus giganteus ND001631

<220>  
 <221> misc\_feature  
 <222> (1)..(213)  
 <223> y is c o r t

<400> 19  
 aaactcggag tacgtctgga acaagtgccg gcctcnggcr gctgggtacc gtcttcgtcc 60  
 gacagacagc asgtgctgtc gtaccggttg cgacgagctg ttcgaggtay cgtcggactc 120  
 ryctccgggm ttcacccaga tkatcacgtc tatgasyggg ttgcccgtgt tcgtcctcat 180  
 ggcgcgtgcc gaagccgttg cccttgatgt tgc 213

<210> 20  
 <211> 71  
 <212> PRT  
 <213> Meripilus giganteus ND001631 enzyme

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(71)  
 <223> x is any amino acid

<400> 20

Ala Thr Ser Arg Ala Thr Ala Ser Ala Arg Ala Met Arg Thr Asn Thr  
 1 5 10 15

Gly Asn Pro Xaa Ile Asp Val Ile Ile Trp Val Xaa Pro Gly Xaa Glu  
 20 25 30

Ser Asp Xaa Thr Ser Asn Ser Ser Ser Xaa Pro Val Arg Gln His Xaa

## Sequence Listing CBH 10377-WO.ST25

35

40

45

Leu Ser Val Gly Arg Arg Arg Tyr Pro Ala Ala Xaa Gly Arg His Leu  
 50 55 60

Phe Gln Thr Tyr Ser Glu Phe  
 65 70

<210> 21  
 <211> 782  
 <212> DNA  
 <213> Trichophaea saccata NP000960

<220>  
 <221> CDS  
 <222> (43)..(702)

<400> 21  
 ggcacgaggg cagatcgatc gactcgagga ccacatcgca tc atg aag aac ttc 54  
 Met Lys Asn Phe  
 1

ctt ctg gcg tcc gcg ctg atc gcg gtt gcc gca gct cag cag agt gct 102  
 Leu Leu Ala Ser Ala Leu Ile Ala Val Ala Ala Gln Gln Ser Ala  
 5 10 15 20

tgg gga cag tgc ggt gga att ggc tgg act ggc gcg acg act tgt atc 150  
 Trp Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Ala Thr Thr Cys Ile  
 25 30 35

tct ggc tac acg tgc tca aag atc aac gac tac tat tcc cag tgc att 198  
 Ser Gly Tyr Thr Cys Ser Lys Ile Asn Asp Tyr Tyr Ser Gln Cys Ile  
 40 45 50

ccg ggt acg gct tca acc acc act caa ggc ggc ggc aat ggc gga gga 246  
 Pro Gly Thr Ala Ser Thr Thr Thr Gln Gly Gly Gly Asn Gly Gly Gly  
 55 60 65

aac ggc ggt aca acg act act ccc act acc act cca gcg gcc agt aac 294  
 Asn Gly Gly Thr Thr Thr Pro Thr Thr Thr Pro Ala Ala Ser Asn  
 70 75 80

acc aac aac ccg ttc tcc ggc aag acc caa tgg gcg aac cct tac tac 342  
 Thr Asn Asn Pro Phe Ser Gly Lys Thr Gln Trp Ala Asn Pro Tyr Tyr  
 85 90 95 100

gct tcc gag gtc tcg agc atc gcc atc ccg tcc ctc gtt gcc gcc gga 390  
 Ala Ser Glu Val Ser Ser Ile Ala Ile Pro Ser Leu Val Ala Ala Gly  
 105 110 115

aac acc cac tac atc gtc gac caa ggc cgc agc ggc aag cag ccg acc 438  
 Asn Thr His Tyr Ile Val Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr  
 120 125 130

ggc cag ctc cag cag ggc gat tgg tgc aac gcc ctg gga acc ggc ttt 486  
 Gly Gln Leu Gln Gln Gly Asp Trp Cys Asn Ala Leu Gly Thr Gly Phe  
 135 140 145

gga att cgt cct gat aca acc ccg gat gat ccc aac ctt gat gct ttc 534  
 Gly Ile Arg Pro Asp Thr Thr Pro Asp Asp Pro Asn Leu Asp Ala Phe  
 150 155 160

gtg tgg gtt aag ccg ggt ggt gaa tcg gat ggt acc agc aat act tcc 582  
 Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asn Thr Ser

Sequence Listing CBH 10377-WO.ST25

165	170	175	180	
tcg acc cgc tat gat tat cat tgt gga cag agc gat gcg cta caa ccg				630
Ser Thr Arg Tyr Asp Tyr His Cys Gly Gln Ser Asp Ala Leu Gln Pro	185	190	195	
gcc ccg gag gcg gga acg tgg ttc cag gcg tat ttt gtg cag ttg ctg				678
Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu	200	205	210	
cag aat gct aat cct agc ttc acg taagcttggg agcgtggggg ttggaagatg				732
Gln Asn Ala Asn Pro Ser Phe Thr	215	220		
tgtattgtat gtgtagatag agaaaaactg ttggcctatt caggactaag				782

<210> 22  
 <211> 220  
 <212> PRT  
 <213> Trichophaea saccata NP000960

<400> 22

Met Lys Asn Phe Leu Leu Ala Ser Ala Leu Ile Ala Val Ala Ala Ala  
 1 5 10 15

Gln Gln Ser Ala Trp Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Ala  
 20 25 30

Thr Thr Cys Ile Ser Gly Tyr Thr Cys Ser Lys Ile Asn Asp Tyr Tyr  
 35 40 45

Ser Gln Cys Ile Pro Gly Thr Ala Ser Thr Thr Thr Gln Gly Gly Gly  
 50 55 60

Asn Gly Gly Gly Asn Gly Gly Thr Thr Thr Thr Pro Thr Thr Thr Pro  
 65 70 75 80

Ala Ala Ser Asn Thr Asn Asn Pro Phe Ser Gly Lys Thr Gln Trp Ala  
 85 90 95

Asn Pro Tyr Tyr Ala Ser Glu Val Ser Ser Ile Ala Ile Pro Ser Leu  
 100 105 110

Val Ala Ala Gly Asn Thr His Tyr Ile Val Asp Gln Gly Arg Ser Gly  
 115 120 125

Lys Gln Pro Thr Gly Gln Leu Gln Gln Gly Asp Trp Cys Asn Ala Leu  
 130 135 140

Gly Thr Gly Phe Gly Ile Arg Pro Asp Thr Thr Pro Asp Asp Pro Asn  
 145 150 155 160

Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr  
 165 170 175

Ser Asn Thr Ser Ser Thr Arg Tyr Asp Tyr His Cys Gly Gln Ser Asp  
180 185 190

Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe  
195 200 205

Val Gln Leu Leu Gln Asn Ala Asn Pro Ser Phe Thr  
210 215 220

```
<210> 23
<211> 1587
<212> DNA
<213> Stibella annulata NP001040
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<220>  
<221> CDS  
<222> (21) .. (1394)

[illegible]

Sequence Listing CBH 10377-WO.ST25																
Gly	Gly	Asn	Tyr 175	Ala	Ser	Ile	Leu	Val 180	Val	Tyr	Asn	Leu	Pro 185	Asp	Arg	
gac Asp	tgc Cys	gcc Ala 190	gcc Ala	gcc Ala	gcc Ala	tcg Ser	aac Asn 195	ggc Gly	gag Glu	ttc Phe	gcc Ala	atc Ile 200	gcc Ala	gac Asp	ggc Gly	629
ggt Gly	gtt Val 205	gct Ala	aag Lys	tac Tyr	aag Lys	aac Asn 210	tac Tyr	att Ile	gac Asp	gag Glu	att Ile 215	cgc Arg	aag Lys	ctc Leu	gtc Val	677
atc Ile 220	aag Lys	tac Tyr	aac Asn	gac Asp	ctc Leu 225	cgt Arg	atc Ile	atc Ile	ctg Leu	gtc Val 230	atc Ile	gag Glu	ccc Pro	gac Asp	tcc Ser 235	725
ctc Leu	gcc Ala	aac Asn	atg Met	gtg Val 240	acc Thr	aac Asn	atg Met	aac Asn	gtc Val 245	gcc Ala	aag Lys	tgc Cys	cag Gln	aac Asn 250	gcc Ala	773
gcc Ala	tcg Ser	gcc Ala	tac Tyr 255	cgg Arg	gag Glu	tgc Cys	acc Thr	aac Asn 260	tat Tyr	gcc Ala	ctg Leu	acg Thr	aac Asn 265	ctc Leu	gac Asp	821
ctg Leu	ccc Pro	aac Asn 270	gtc Val	gcc Ala	cag Gln	tac Tyr	atg Met 275	gat Asp	gcc Ala	gga Gly	cat His	gct Ala 280	ggc Gly	tgg Trp	ctc Leu	869
ggc Gly	tgg Trp 285	ccc Pro	gcc Ala	aac Asn	atc Ile	acc Thr 290	ccc Pro	gcc Ala	gcc Ala	cag Gln	ctc Leu 295	ttc Phe	gcc Ala	gag Glu	gtc Val	917
tac Tyr 300	aag Lys	cag Gln	gcc Ala	ggc Gly	agc Ser 305	ccc Pro	aag Lys	tcg Ser	gtc Val	cgt Arg 310	ggc Gly	ctg Leu	gcc Ala	atc Ile	aac Asn 315	965
gtc Val	tcc Ser	aac Asn	tac Tyr	aac Asn 320	gcg Ala	tgg Trp	agc Ser	gtt Val	tcg Ser 325	tcc Ser	cct Pro	cct Pro	ccc Pro	tac Tyr 330	acc Thr	1013
tct Ser	ccc Pro	aac Asn	ccc Pro 335	aac Asn	tac Tyr	gac Asp	gag Glu	cgc Arg 340	cac His	ttc Phe	gtt Val	gag Glu	gcc Ala 345	ttt Phe	gcg Ala	1061
ccc Pro	ctc Leu	ctg Leu 350	cgc Arg	cag Gln	aac Asn	ggc Gly	tgg Trp 355	gat Asp	gcc Ala	aag Lys	ttc Phe	atc Ile 360	gtc Val	gac Asp	cag Gln	1109
ggc Gly	cgc Arg 365	tcc Ser	ggc Gly	agg Arg	cag Gln	ccc Pro 370	acc Thr	ggc Gly	cag Gln	cag Gln	gag Glu 375	tgg Trp	gga Gly	cac His	tgg Trp	1157
tgc Cys 380	aac Asn	gcc Ala	atc Ile	ggc Gly	act Thr 385	ggc Gly	ttc Phe	ggc Gly	cag Gln	cgc Arg 390	ccg Pro	acg Thr	tcc Ser	aac Asn	acc Thr 395	1205
ggc Gly	cac His	gcc Ala	gat Asp	gtt Val 400	gac Asp	gct Ala	ttc Phe	gtc Val	tgg Trp 405	atc Ile	aag Lys	ccg Pro	ggc Gly	ggc Gly 410	gag Glu	1253
tgc Cys	gac Asp	ggc Gly	acc Thr 415	agc Ser	gac Asp	acc Thr	tcg Ser	gcc Ala 420	gcc Ala	cgc Arg	tac Tyr	gac Asp	cac His 425	ttc Phe	tgt Cys	1301
ggc Gly	aac Asn	cct Pro 430	gat Asp	gcc Ala	ctc Leu	aag Lys	ccg Pro 435	gcc Ala	ccc Pro	gaa Glu	gcc Ala	gga Gly 440	gag Glu	tgg Trp	ttc Phe	1349
cag	gcc	tac	ttc	gag	cag	ctt	ctg	cgc	aac	gcc	aac	ccc	gcc	ttc		1394

## Sequence Listing CBH 10377-WO.ST25

Gln Ala Tyr Phe Glu Gln Leu Leu Arg Asn Ala Asn Pro Ala Phe  
 445 450 455

taagtgtctg atgagctttt ctgagagggt acttccgcgg tcttgggttt cactcttctc 1454  
 agcctttcag ggcagcagtt ttggtttctt ggggtaggac ctccgggttt atgtagacgg 1514  
 agttaggaag ccaaactac tatgaatgta gtattcaaga agataatgac ttgaaaaaaaa 1574  
 aaaaaaaaaa aaa 1587

&lt;210&gt; 24

&lt;211&gt; 458

&lt;212&gt; PRT

&lt;213&gt; Stibella annulata NP001040

&lt;400&gt; 24

Met Ala Gly Arg Phe Phe Leu Ser Ala Ala Phe Leu Ala Ser Ala Ala  
 1 5 10 15

Leu Ala Val Pro Leu Glu Glu Arg Gln Asn Cys Ser Pro Gln Trp Ala  
 20 25 30

Gln Cys Gly Gly Asn Gly Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly  
 35 40 45

Ser Asn Cys Gln Val Thr Asn Glu Trp Tyr Ser Gln Cys Val Pro Gly  
 50 55 60

Ala Ala Pro Pro Pro Pro Pro Val Thr Thr Thr Arg Ser Thr Thr Thr  
 65 70 75 80

Pro Pro Thr Thr Thr Thr Arg Thr Thr Ala Asp Ala Pro Pro Pro Thr  
 85 90 95

Gly Gly Ala Thr Tyr Thr Gly Asn Pro Phe Leu Gly Val Asn Gln Trp  
 100 105 110

Ala Asn Asn Phe Tyr Arg Ser Glu Ile Met Asn Ile Ala Val Pro Ser  
 115 120 125

Leu Ser Gly Ala Met Ala Thr Ala Ala Ala Lys Val Ala Asp Val Pro  
 130 135 140

Thr Phe Gln Trp Ile Asp Lys Met Asp Lys Leu Pro Leu Ile Asp Glu  
 145 150 155 160

Ala Leu Ala Asp Val Arg Ala Ala Asn Ala Arg Gly Gly Asn Tyr Ala  
 165 170 175

Ser Ile Leu Val Val Tyr Asn Leu Pro Asp Arg Asp Cys Ala Ala Ala  
 180 185 190

Ala Ser Asn Gly Glu Phe Ala Ile Ala Asp Gly Gly Val Ala Lys Tyr



## Sequence Listing CBH 10377-WO.ST25

195

200

205

Lys Asn Tyr Ile Asp Glu Ile Arg Lys Leu Val Ile Lys Tyr Asn Asp  
 210 215 220

Leu Arg Ile Ile Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Met Val  
 225 230 235 240

Thr Asn Met Asn Val Ala Lys Cys Gln Asn Ala Ala Ser Ala Tyr Arg  
 245 250 255

Glu Cys Thr Asn Tyr Ala Leu Thr Asn Leu Asp Leu Pro Asn Val Ala  
 260 265 270

Gln Tyr Met Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn  
 275 280 285

Ile Thr Pro Ala Ala Gln Leu Phe Ala Glu Val Tyr Lys Gln Ala Gly  
 290 295 300

Ser Pro Lys Ser Val Arg Gly Leu Ala Ile Asn Val Ser Asn Tyr Asn  
 305 310 315 320

Ala Trp Ser Val Ser Ser Pro Pro Pro Tyr Thr Ser Pro Asn Pro Asn  
 325 330 335

Tyr Asp Glu Arg His Phe Val Glu Ala Phe Ala Pro Leu Leu Arg Gln  
 340 345 350

Asn Gly Trp Asp Ala Lys Phe Ile Val Asp Gln Gly Arg Ser Gly Arg  
 355 360 365

Gln Pro Thr Gly Gln Gln Glu Trp Gly His Trp Cys Asn Ala Ile Gly  
 370 375 380

Thr Gly Phe Gly Gln Arg Pro Thr Ser Asn Thr Gly His Ala Asp Val  
 385 390 395 400

Asp Ala Phe Val Trp Ile Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser  
 405 410 415

Asp Thr Ser Ala Ala Arg Tyr Asp His Phe Cys Gly Asn Pro Asp Ala  
 420 425 430

Leu Lys Pro Ala Pro Glu Ala Gly Glu Trp Phe Gln Ala Tyr Phe Glu  
 435 440 445

Gln Leu Leu Arg Asn Ala Asn Pro Ala Phe  
 450 455

&lt;210&gt; 25

## Sequence Listing CBH 10377-WO.ST25

<211> 1559  
<212> DNA  
<213> Malbrancheae cinnamonea NP001045

$\langle 220 \rangle$   
 $\langle 221 \rangle$  CDS  
 $\langle 222 \rangle$  (41) .. (1210)

[illegible]

Sequence Listing CBH 10377-WO.ST25																		
215				220													225	
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acg Thr	aac Asn	gtt Val	tcc Ser	aac Asn 250	tac Tyr	aac Asn	ggt Gly	tat Tyr	tcc Ser 255	ctc Leu	agc Ser	acc Thr	gct Ala	cct Pro 260	ccc Pro	823		
tac Tyr	act Thr	gag Glu	ccc Pro 265	aac Asn	ccc Pro	aat Asn	ttc Phe	gac Asp 270	gaa Glu	gtg Val	cgt Arg	tat Tyr	atc Ile 275	aat Asn	gca Ala	871		
ttc Phe	cgc Arg	cca Pro 280	ctc Leu	ctc Leu	gag Glu	gca Ala	cgg Arg 285	ggt Gly	ttc Phe	cca Pro	gca Ala	tac Tyr 290	ttc Phe	atc Ile	gtc Val	919		
gac Asp	caa Gln 295	ggc Gly	cgc Arg	agc Ser	ggt Gly	gtc Val 300	cag Gln	ccc Pro	act Thr	gcg Ala	cag Gln 305	att Ile	gag Glu	caa Gln	gga Gly	967		
cac His 310	tgg Trp	tgc Cys	aat Asn	gtg Val	atc Ile 315	gac Asp	acc Thr	ggt Gly	ttt Phe	gga Gly 320	act Thr	cgc Arg	ccc Pro	act Thr	act Thr 325	1015		
gac Asp	act Thr	ggt Gly	aat Asn	gag Glu 330	tac Tyr	gtt Val	gac Asp	tcg Ser	atc Ile 335	gtg Val	tgg Trp	gtg Val	aag Lys	cct Pro 340	ggc Gly	1063		
ggc Gly	gaa Glu	tcg Ser	gac Asp 345	gga Gly	acc Thr	agc Ser	gat Asp	acc Thr 350	tct Ser	gct Ala	gag Glu	aga Arg	tat Tyr 355	gac Asp	tac Tyr	1111		
cac His	tgc Cys	gga Gly 360	ctt Leu	gag Glu	gat Asp	gca Ala	ttg Leu 365	aag Lys	cca Pro	gct Ala	cct Pro	gaa Glu 370	gcg Ala	gga Gly	cag Gln	1159		
tgg Trp	ttc Phe 375	cag Gln	gcc Ala	tac Tyr	ttc Phe	gag Glu 380	caa Gln	ctg Leu	ctc Leu	aga Arg	aat Asn 385	gcc Ala	aac Asn	ccc Pro	cca Pro	1207		
ttc taaatcagat gaaggacgga cccaattgat gacggcctgt cttcgtgac																1260		
Phe																		
390																		
cgacgaaagc aatgtcaggg tgaaaatgac cgagagattg gagagtcattg aggataggta																1320		
gtcaatgatt tcacccgagt ttccacgttt tacccttctt gtacatagtt tggagtcgcc																1380		
tgttggtttc agtagtacat cttatccgac agagtctatc gtttgattac cccagtcaaa																1440		
agcgttattg caatcttttc ctagggattt attgtttgct gcggatgtcg tggctatggg																1500		
cagctgactg aattaaactg gaactcttgg tatccaaaaa aaaaaaaaaa aaaaaaaaaa																1559		
<210> 26																		
<211> 390																		
<212> PRT																		
<213> Malbrancheae cinnamonea NP001045																		
<400> 26																		
Met Arg Asp Ser Leu Phe Thr Leu Leu Ser Leu Ala Leu Gly Ser Ala																		
1 5 10 15																		

## Sequence Listing CBH 10377-WO.ST25

Ser Ala Ser Pro Phe Leu Leu Pro Arg Gln Ala Asn Ser Ser Asn Pro  
 20 25 30  
 Phe Ala Gly His Thr Ile Tyr Pro Asn Pro Tyr Tyr Ser Asn Glu Ile  
 35 40 45  
 Asp Glu Phe Ala Ile Pro Ala Leu Gln Glu Thr Asp Pro Ala Leu Val  
 50 55 60  
 Glu Lys Ala Ala Leu Val Lys Glu Val Gly Thr Phe Phe Trp Ile Asp  
 65 70 75 80  
 Val Val Ala Lys Val Pro Asp Ile Gly Pro Tyr Leu Gln Gly Ile Gln  
 85 90 95  
 Glu Ala Asn Ala Ala Gly Gln Asn Pro Pro Tyr Ile Gly Ala Ile Val  
 100 105 110  
 Val Tyr Asp Leu Pro Asn Arg Asp Cys Ala Ala Ala Ala Ser Asn Gly  
 115 120 125  
 Glu Phe Ser Leu Glu Asp Gly Gly Glu Glu Lys Tyr Arg Gly Tyr Ile  
 130 135 140  
 Asp Gly Ile Arg Glu Gln Ile Glu Lys Tyr Pro Asp Val Arg Val Ala  
 145 150 155 160  
 Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Met Val Thr Asn Leu Asn  
 165 170 175  
 Val Pro Lys Cys Ala Glu Ser Glu Gln Ala Tyr Arg Asp Gly Val Ala  
 180 185 190  
 Tyr Ala Leu Lys Gln Leu Asp Leu Pro Asn Val Trp Thr Tyr Ile Asp  
 195 200 205  
 Ala Gly His Ser Gly Trp Leu Gly Trp Pro Ala Asn Ile Glu Pro Ala  
 210 215 220  
 Ala Glu Ile Phe Val Glu Val Trp Asn Ala Ala Gly Arg Pro Lys Ser  
 225 230 235 240  
 Thr Arg Gly Phe Ala Thr Asn Val Ser Asn Tyr Asn Gly Tyr Ser Leu  
 245 250 255  
 Ser Thr Ala Pro Pro Tyr Thr Glu Pro Asn Pro Asn Phe Asp Glu Val  
 260 265 270  
 Arg Tyr Ile Asn Ala Phe Arg Pro Leu Leu Glu Ala Arg Gly Phe Pro  
 275 280 285

## Sequence Listing CBH 10377-WO.ST25

Ala Tyr Phe Ile Val Asp Gln Gly Arg Ser Gly Val Gln Pro Thr Ala  
 290 295 300

Gln Ile Glu Gln Gly His Trp Cys Asn Val Ile Asp Thr Gly Phe Gly  
 305 310 315 320

Thr Arg Pro Thr Thr Asp Thr Gly Asn Glu Tyr Val Asp Ser Ile Val  
 325 330 335

Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala  
 340 345 350

Glu Arg Tyr Asp Tyr His Cys Gly Leu Glu Asp Ala Leu Lys Pro Ala  
 355 360 365

Pro Glu Ala Gly Gln Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu Arg  
 370 375 380

Asn Ala Asn Pro Pro Phe  
 385 390

<210> 27  
 <211> 17  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Primer

<220>  
 <221> misc\_feature  
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 <223> r is a or g

y is t or c

n is a, g, t, or c

<400> 27  
 tggggncart gyggngg

17

<210> 28  
 <211> 17  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Primer

<220>  
 <221> misc\_feature  
 <222> (1)..(17)  
 <223> y is t or c

n is a, g, t, or c

<400> 28  
 tggytnggnt ggccngc

17

## Sequence Listing CBH 10377-WO.ST25

<210> 29  
<211> 17  
<212> DNA  
<213> Artificial

<220>  
<223> Primer

<220>  
<221> misc\_feature  
<222> (1)..(17)  
<223> n is a, g, t, or c.

r is a or g

<400> 29  
gcnggccanc cnarcca

17

<210> 30  
<211> 17  
<212> DNA  
<213> Artificial

<220>  
<223> Primer

<220>  
<221> misc\_feature  
<222> (1)..(17)  
<223> r is a or g

n is a, g, t, or c

<400> 30  
ttrcaccart cncccca

17

<210> 31  
<211> 17  
<212> DNA  
<213> Artificial

<220>  
<223> Primer

<220>  
<221> misc\_feature  
<222> (1)..(17)  
<223> r is a or g

y is t or c

n is a, g, t or c

<400> 31  
ggyttnaccc anacraa

17

<210> 32  
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<212> DNA  
<213> Artificial

## Sequence Listing CBH 10377-WO.ST25

&lt;220&gt;

&lt;223&gt; Primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(17)

&lt;223&gt; r is a or g

y is t or c

n is a, g, t or c

&lt;400&gt; 32

aartangcyt graacca

17

&lt;210&gt; 33

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(25)

&lt;400&gt; 33

gggtcatgag agactctttg ttcac

25

&lt;210&gt; 34

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(34)

&lt;400&gt; 34

gggttaatta attagaatgg ggggttgga tttc

34

&lt;210&gt; 35

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 35

actggattta ccatggccgg tcgattcttc c

31

&lt;210&gt; 36

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial

Sequence Listing CBH 10377-WO.ST25

<220>

<223> Primer

<400> 36

agtcacctct agttattaga aggcgggggtt g

31